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TERMINAL (ENTER 1, 2, 3, OR ?):2

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NEWS	1		Web Page URLs for STN Seminar Schedule - N. America
NEWS	2		"Ask CAS" for self-help around the clock
NEWS	3	DEC 21	IPC search and display fields enhanced in CA/CAPLUS with the IPC reform
NEWS	4	DEC 23	New IPC8 SEARCH, DISPLAY, and SELECT fields in USPATFULL/USPAT2
NEWS	5	JAN 13	IPC 8 searching in IFIPAT, IFIUDB, and IFICDB
NEWS	6	JAN 13	New IPC 8 SEARCH, DISPLAY, and SELECT enhancements added to INPADOC
NEWS	7	JAN 17	Pre-1988 INPI data added to MARPAT
NEWS	8	JAN 17	IPC 8 in the WPI family of databases including WPIFV
NEWS	9	JAN 30	Saved answer limit increased
NEWS	10	JAN 31	Monthly current-awareness alert (SDI) frequency added to TULSA
NEWS	11	FEB 21	STN AnaVist, Version 1.1, lets you share your STN AnaVist visualization results
NEWS	12	FEB 22	Status of current WO (PCT) information on STN
NEWS	13	FEB 22	The IPC thesaurus added to additional patent databases on STN
NEWS	14	FEB 22	Updates in EPFULL; IPC 8 enhancements added
NEWS	15	FEB 27	New STN AnaVist pricing effective March 1, 2006
NEWS	16	FEB 28	MEDLINE/LMEDLINE reload improves functionality
NEWS	17	FEB 28	TOXCENTER reloaded with enhancements
NEWS	18	FEB 28	REGISTRY/ZREGISTRY enhanced with more experimental spectral property data
NEWS	19	MAR 01	INSPEC reloaded and enhanced
NEWS	20	MAR 03	Updates in PATDPA; addition of IPC 8 data without attributes
NEWS	21	MAR 08	X.25 communication option no longer available after June 2006
NEWS	22	MAR 22	EMBASE is now updated on a daily basis

NEWS EXPRESS FEBRUARY 15 CURRENT VERSION FOR WINDOWS IS V8.01a,
CURRENT MACINTOSH VERSION IS V6.0c(ENG) AND V6.0Jc(JP),
AND CURRENT DISCOVER FILE IS DATED 19 DECEMBER 2005.
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FILE 'HOME' ENTERED AT 10:40:31 ON 28 MAR 2006

=> file reg		
COST IN U.S. DOLLARS	SINCE FILE	TOTAL
	ENTRY	SESSION
FULL ESTIMATED COST	0.21	0.21

FILE 'REGISTRY' ENTERED AT 10:40:42 ON 28 MAR 2006
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* effective March 20, 2005. A new display format, IDERL, is now *
* available and contains the CA role and document type information. *
*

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<http://www.cas.org/ONLINE/UG/regprops.html>

```
=> s TGAAATGCTCA/SQEN
      2 TGAAATGCTCA/SQEN
      87009 SQL=11
L1      2 TGAAATGCTCA/SQEN
      (TGAAATGCTCA/SQEN AND SQL=11)
```

=> file caplus		
COST IN U.S. DOLLARS	SINCE FILE	TOTAL
	ENTRY	SESSION
FULL ESTIMATED COST	7.93	8.14

FILE 'CAPLUS' ENTERED AT 10:41:37 ON 28 MAR 2006
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FILE COVERS 1907 - 28 Mar 2006 VOL 144 ISS 14
FILE LAST UPDATED: 27 Mar 2006 (20060327/ED)

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=> s l1

L2 1 L1

=> d ibib

L2 ANSWER 1 OF 1 CAPLUS COPYRIGHT 2006 ACS on STN

ACCESSION NUMBER: 2001:208447 CAPLUS

DOCUMENT NUMBER: 134:247984

TITLE: Polymorphisms in the human CYP3A4 and CYP3A7 genes and their use in diagnostic and therapeutic applications

INVENTOR(S): Wojnowski, Leszek; Eiselt, Regina

PATENT ASSIGNEE(S): Epidauros Biotechnologie A.-G., Germany

SOURCE: PCT Int. Appl., 106 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 3

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001020025	A2	20010322	WO 2000-EP8570	20000901
WO 2001020025	A3	20011011		
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
RW:	GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG			
EP 1088900	A1	20010404	EP 1999-118120	19990910
R:	AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO			
CA 2379541	AA	20010322	CA 2000-2379541	20000901
EP 1210463	A2	20020605	EP 2000-964092	20000901
R:	AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL			
JP 2003509063	T2	20030311	JP 2001-523796	20000901

US 2002160479	A1	20021031	US 2001-7814	20011109
NO 2002001146	A	20020415	NO 2002-1146	20020307
PRIORITY APPLN. INFO.:			EP 1999-118120	A 19990910
			US 2000-583447	A3 20000530
			WO 2000-EP8570	W 20000901

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=> file reg
COST IN U.S. DOLLARS          SINCE FILE          TOTAL
                                ENTRY          SESSION
FULL ESTIMATED COST          1.60          9.74
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FILE 'REGISTRY' ENTERED AT 10:42:18 ON 28 MAR 2006
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TSCA INFORMATION NOW CURRENT THROUGH January 6, 2006

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```
*****
*
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* the IDE default display format and the ED field has been added, *
* effective March 20, 2005. A new display format, IDERL, is now *
* available and contains the CA role and document type information. *
*
*****
```

Structure search iteration limits have been increased. See HELP SLIMITS
 for details.

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 predicted properties as well as tags indicating availability of
 experimental property data in the original document. For information
 on property searching in REGISTRY, refer to:

<http://www.cas.org/ONLINE/UG/regprops.html>

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=> s TGAAATGCTCA/SQSN
L3      26979 TGAAATGCTCA/SQSN
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=> s l3 and SQL<=50
      7659901 SQL<=50
L4      13 L3 AND SQL<=50
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=> file caplus
COST IN U.S. DOLLARS          SINCE FILE          TOTAL
                                ENTRY          SESSION
FULL ESTIMATED COST          34.53          44.27
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FILE 'CAPLUS' ENTERED AT 10:44:00 ON 28 MAR 2006

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FILE COVERS 1907 - 28 Mar 2006 VOL 144 ISS 14
FILE LAST UPDATED: 27 Mar 2006 (20060327/ED)

Effective October 17, 2005, revised CAS Information Use Policies apply. They are available for your review at:

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=> s 14

L5 10 L4

=> s 15 not py>1999

6510150 PY>1999

L6 0 L5 NOT PY>1999

=> d 15 ibib 7-10

L5 ANSWER 7 OF 10 CAPLUS COPYRIGHT 2006 ACS on STN

ACCESSION NUMBER: 2004:633637 CAPLUS

DOCUMENT NUMBER: 141:152173

TITLE: Method and oligonucleotide probes for genotyping polymorphisms in humans

INVENTOR(S): Matsuzaki, Hajime; Mei, Rui; Shen, Mei-Mei; Kennedy, Giulia C.

PATENT ASSIGNEE(S): Affymetrix, Inc., USA

SOURCE: U.S. Pat. Appl. Publ., 13 pp.

CODEN: USXXCO

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 26

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2004146890	A1	20040729	US 2003-681773	20031007
US 2004146890	A1	20040729	US 2003-681773	20031007
PRIORITY APPLN. INFO.:			US 2002-417190P	P 20021008
			US 2003-470475P	P 20030514
			US 2003-681773	A 20031007

L5 ANSWER 8 OF 10 CAPLUS COPYRIGHT 2006 ACS on STN

ACCESSION NUMBER: 2004:120997 CAPLUS

DOCUMENT NUMBER: 140:158538

TITLE: Methods for detecting PrP gene polymorphisms associated with scrapie in sheep using primer extension

INVENTOR(S): Mckeown, Brian; Derbyshire, Roger; Rowan, Paul; Sung,

PATENT ASSIGNEE(S): Robert
 SOURCE: Orchid Biosciences, Inc., USA
 PCT Int. Appl., 121 pp.
 CODEN: PIXXD2
 DOCUMENT TYPE: Patent
 LANGUAGE: English
 FAMILY ACC. NUM. COUNT: 2
 PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2004013346	A2	20040212	WO 2003-US24198	20030801
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, UZ, VC, VN, YU, ZA, ZM, ZW RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
US 2004121342	A1	20040624	US 2002-328150	20021220
CA 2497570	AA	20040212	CA 2003-2497570	20030801
EP 1576174	A2	20050921	EP 2003-767088	20030801
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR, BG, CZ, EE, HU, SK				
PRIORITY APPLN. INFO.:			US 2002-400533P	P 20020802
			US 2002-328150	A 20021220
			WO 2003-US24198	W 20030801

L5 ANSWER 9 OF 10 CAPLUS COPYRIGHT 2006 ACS on STN
 ACCESSION NUMBER: 2001:208447 CAPLUS
 DOCUMENT NUMBER: 134:247984
 TITLE: Polymorphisms in the human CYP3A4 and CYP3A7 genes and
 their use in diagnostic and therapeutic applications
 INVENTOR(S): Wojnowski, Leszek; Eiselt, Regina
 PATENT ASSIGNEE(S): Epidauros Biotechnologie A.-G., Germany
 SOURCE: PCT Int. Appl., 106 pp.
 CODEN: PIXXD2
 DOCUMENT TYPE: Patent
 LANGUAGE: English
 FAMILY ACC. NUM. COUNT: 3
 PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001020025	A2	20010322	WO 2000-EP8570	20000901
WO 2001020025	A3	20011011		
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
EP 1088900	A1	20010404	EP 1999-118120	19990910
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO				
CA 2379541	AA	20010322	CA 2000-2379541	20000901

EP 1210463	A2	20020605	EP 2000-964092	20000901
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL				
JP 2003509063	T2	20030311	JP 2001-523796	20000901
US 2002160479	A1	20021031	US 2001-7814	20011109
NO 2002001146	A	20020415	NO 2002-1146	20020307
PRIORITY APPLN. INFO.:			EP 1999-118120	A 19990910
			US 2000-583447	A3 20000530
			WO 2000-EP8570	W 20000901

L5 ANSWER 10 OF 10 CAPLUS COPYRIGHT 2006 ACS on STN

ACCESSION NUMBER: 2000:707338 CAPLUS

DOCUMENT NUMBER: 133:291967

TITLE: Single nucleotide polymorphisms in coding regions of human genes and primers/probes and methods for detection thereof

INVENTOR(S): Altshuler, David; Cargill, Michele; Daley, George Q.; Ireland, James S.; Lander, Eric S.; Lipshutz, Robert J.; Patil, Nila; Sklar, Pamela

PATENT ASSIGNEE(S): Whitehead Institute for Biomedical Research, USA; Affymetrix, Inc.

SOURCE: PCT Int. Appl., 216 pp.
CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
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WO 2000058519	A2	20001005	WO 2000-US8440	20000330
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
PRIORITY APPLN. INFO.:			US 1999-127248P	P 19990331

=>

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=>

Executing the logoff script...

=> LOG Y

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NEWS 14 FEB 22 Updates in EPFULL; IPC 8 enhancements added
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NEWS 21 MAR 08 X.25 communication option no longer available after June 2006
NEWS 22 MAR 22 EMBASE is now updated on a daily basis

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=> file re

'RE' IS AN AMBIGUOUS FILE OR CLUSTER NAME

REACTION - Reactions Cluster

RESEARCH - Research Cluster
REGISTRY - The CAS Registry File of substances
ENTER FILE OR CLUSTER NAME (IGNORE):end

```
=> file reg
COST IN U.S. DOLLARS          SINCE FILE      TOTAL
                               ENTRY      SESSION
FULL ESTIMATED COST          0.21          0.21
```

FILE 'REGISTRY' ENTERED AT 11:35:24 ON 28 MAR 2006
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STRUCTURE FILE UPDATES: 27 MAR 2006 HIGHEST RN 878190-58-0
DICTIONARY FILE UPDATES: 27 MAR 2006 HIGHEST RN 878190-58-0

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* the IDE default display format and the ED field has been added,   *
* effective March 20, 2005. A new display format, IDERL, is now      *
* available and contains the CA role and document type information. *
*
*****
```

Structure search iteration limits have been increased. See HELP SLIMITS
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on property searching in REGISTRY, refer to:

<http://www.cas.org/ONLINE/UG/regprops.html>

```
=> s TGAAATGCTCA/SQSN
L1      26979 TGAAATGCTCA/SQSN
```

```
=> s l1 and SQL,+50
          0 SQL,+50
L2      0 L1 AND SQL,+50
```

```
=> s l1 and SQL<=50
          7659901 SQL<=50
L3      13 L1 AND SQL<=50
```

```
=> file caplus
COST IN U.S. DOLLARS          SINCE FILE      TOTAL
                               ENTRY      SESSION
FULL ESTIMATED COST          39.29          39.50
```

FILE 'CAPLUS' ENTERED AT 11:36:59 ON 28 MAR 2006
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FILE LAST UPDATED: 27 Mar 2006 (20060327/ED)

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<http://www.cas.org/infopolicy.html>

=> s 13
L4 10 L3

=> d ibib 1-10

L4 ANSWER 1 OF 10 CAPLUS COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER: 2005:1154714 CAPLUS
DOCUMENT NUMBER: 143:438059
TITLE: Genetic polymorphisms in 11 genes associated with an increased risk of osteoarthritis
INVENTOR(S): Mah, Steven; Braun, Andreas; Kammerer, Stefan M.; Nelson, Matthew Roberts; Reneland, Rikard Henry; Langdown, Maria L.
PATENT ASSIGNEE(S): Sequenom, Inc., USA
SOURCE: PCT Int. Appl., 539 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2005100604	A2	20051027	WO 2005-US10912	20050331
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SM, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM,			ZW
RW:	BW, GH, GM, KE, LS, MW, MZ, NA, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IS, IT, LT, LU, MC, NL, PL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG			
PRIORITY APPLN. INFO.:			US 2004-559011P	P 20040401
			US 2004-559040P	P 20040401
			US 2004-559042P	P 20040401

US 2004-559202P	P	20040401
US 2004-559203P	P	20040401
US 2004-559225P	P	20040401
US 2004-559275P	P	20040401

L4 ANSWER 2 OF 10 CAPLUS COPYRIGHT 2006 ACS on STN
 ACCESSION NUMBER: 2005:1004428 CAPLUS
 DOCUMENT NUMBER: 143:282819
 TITLE: Use of Solanum bulbocastanum genes RB, RGA1 RGA3 and RGA4 for conferring broad spectrum resistance to potato late blight in transgenic solanaceae
 INVENTOR(S): Helgeson, John Paul; Austin-Phillips, Sandra; Naess, Sara Kristine; Song, Junqi; Jiang, Jiming; Bradeen, James Mathew; Buell, C. Rubin
 PATENT ASSIGNEE(S): USA
 SOURCE: U.S. Pat. Appl. Publ., 121 pp.
 CODEN: USXXCO
 DOCUMENT TYPE: Patent
 LANGUAGE: English
 FAMILY ACC. NUM. COUNT: 1
 PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2005204419	A1	20050915	US 2004-755966	20040112
PRIORITY APPLN. INFO.:			US 2003-439376P	P 20030110

L4 ANSWER 3 OF 10 CAPLUS COPYRIGHT 2006 ACS on STN
 ACCESSION NUMBER: 2005:172216 CAPLUS
 DOCUMENT NUMBER: 142:213372
 TITLE: Oligonucleotide probes for analysis of gene expression in mouse
 INVENTOR(S): Zhou, Xue Mei
 PATENT ASSIGNEE(S): Affymetrix, Inc., USA
 SOURCE: U.S. Pat. Appl. Publ., 13 pp.
 CODEN: USXXCO
 DOCUMENT TYPE: Patent
 LANGUAGE: English
 PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2005026164 A1		20050203	US 2003-XC719900	20031120
PRIORITY APPLN. INFO.:			US 2002-2002/PV42780U	20021120
			US 2003-2003/719900	20031120

L4 ANSWER 4 OF 10 CAPLUS COPYRIGHT 2006 ACS on STN
 ACCESSION NUMBER: 2005:110603 CAPLUS
 DOCUMENT NUMBER: 142:171061
 TITLE: Oligonucleotide probes for analysis of gene expression in mouse
 INVENTOR(S): Zhou, Xue Mei
 PATENT ASSIGNEE(S): Affymetrix, Inc., USA
 SOURCE: U.S. Pat. Appl. Publ., 13 pp.
 CODEN: USXXCO
 DOCUMENT TYPE: Patent
 LANGUAGE: English
 PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2005026164 A1		20050203	US 2003-XS719900	20031120

PRIORITY APPLN. INFO.: US 2002-2002/PV42780U 20021120
US 2003-2003/719900 20031120

L4 ANSWER 5 OF 10 CAPLUS COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER: 2004:701704 CAPLUS
DOCUMENT NUMBER: 141:219946
TITLE: Methods for genotyping scrapie-resistant sheep
populations
INVENTOR(S): McKeown, Brian; Derbyshire, Roger; Rowan, Paul; Sung,
Robert
PATENT ASSIGNEE(S): Orchid Biosciences, Inc., USA
SOURCE: U.S. Pat. Appl. Publ., 64 pp., Cont.-in-part of U.S.
Ser. No. 328,150.
CODEN: USXXCO
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 2
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2004166506	A1	20040826	US 2003-632393	20030801
US 2004121342	A1	20040624	US 2002-328150	20021220
PRIORITY APPLN. INFO.:			US 2002-400533P	P 20020802
			US 2002-328150	A2 20021220

L4 ANSWER 6 OF 10 CAPLUS COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER: 2004:633648 CAPLUS
DOCUMENT NUMBER: 141:135193
TITLE: Method and oligonucleotide probes for genotyping
polymorphisms in humans
INVENTOR(S): Matsuzaki, Hajime; Mei, Rui; Shen, Mei-Mei; Kennedy,
Giulia C.
PATENT ASSIGNEE(S): Affymetrix, Inc., USA
SOURCE: U.S. Pat. Appl. Publ., 13 pp.
CODEN: USXXCO
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 26
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2004146890	A1	20040729	US 2003-681773	20031007
US 2004146890	A1	20040729	US 2003-681773	20031007
PRIORITY APPLN. INFO.:			US 2002-417190P	P 20021008
			US 2003-470475P	P 20030514
			US 2003-681773	A 20031007

L4 ANSWER 7 OF 10 CAPLUS COPYRIGHT 2006 ACS on STN
ACCESSION NUMBER: 2004:633637 CAPLUS
DOCUMENT NUMBER: 141:152173
TITLE: Method and oligonucleotide probes for genotyping
polymorphisms in humans
INVENTOR(S): Matsuzaki, Hajime; Mei, Rui; Shen, Mei-Mei; Kennedy,
Giulia C.
PATENT ASSIGNEE(S): Affymetrix, Inc., USA
SOURCE: U.S. Pat. Appl. Publ., 13 pp.
CODEN: USXXCO
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 26

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2004146890	A1	20040729	US 2003-681773	20031007
US 2004146890	A1	20040729	US 2003-681773	20031007
PRIORITY APPLN. INFO.:			US 2002-417190P	P 20021008
			US 2003-470475P	P 20030514
			US 2003-681773	A 20031007

L4 ANSWER 8 OF 10 CAPLUS COPYRIGHT 2006 ACS on STN

ACCESSION NUMBER: 2004:120997 CAPLUS

DOCUMENT NUMBER: 140:158538

TITLE: Methods for detecting PrP gene polymorphisms associated with scrapie in sheep using primer extension

INVENTOR(S): Mckeown, Brian; Derbyshire, Roger; Rowan, Paul; Sung, Robert

PATENT ASSIGNEE(S): Orchid Biosciences, Inc., USA

SOURCE: PCT Int. Appl., 121 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 2

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2004013346	A2	20040212	WO 2003-US24198	20030801
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, UZ, VC, VN, YU, ZA, ZM, ZW				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
US 2004121342	A1	20040624	US 2002-328150	20021220
CA 2497570	AA	20040212	CA 2003-2497570	20030801
EP 1576174	A2	20050921	EP 2003-767088	20030801
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PRIORITY APPLN. INFO.:			US 2002-400533P	P 20020802
			US 2002-328150	A 20021220
			WO 2003-US24198	W 20030801

L4 ANSWER 9 OF 10 CAPLUS COPYRIGHT 2006 ACS on STN

ACCESSION NUMBER: 2001:208447 CAPLUS

DOCUMENT NUMBER: 134:247984

TITLE: Polymorphisms in the human CYP3A4 and CYP3A7 genes and their use in diagnostic and therapeutic applications

INVENTOR(S): Wojnowski, Leszek; Eiselt, Regina

PATENT ASSIGNEE(S): Epidauros Biotechnologie A.-G., Germany

SOURCE: PCT Int. Appl., 106 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 3

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
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WO 2001020025	A2	20010322	WO 2000-EP8570	20000901
WO 2001020025	A3	20011011		
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
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EP 1088900	A1	20010404	EP 1999-118120	19990910
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CA 2379541	AA	20010322	CA 2000-2379541	20000901
EP 1210463	A2	20020605	EP 2000-964092	20000901
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JP 2003509063	T2	20030311	JP 2001-523796	20000901
US 2002160479	A1	20021031	US 2001-7814	20011109
NO 2002001146	A	20020415	NO 2002-1146	20020307
PRIORITY APPLN. INFO.:			EP 1999-118120	A 19990910
			US 2000-583447	A3 20000530
			WO 2000-EP8570	W 20000901

L4 ANSWER 10 OF 10 CAPLUS COPYRIGHT 2006 ACS on STN

ACCESSION NUMBER: 2000:707338 CAPLUS

DOCUMENT NUMBER: 133:291967

TITLE: Single nucleotide polymorphisms in coding regions of human genes and primers/probes and methods for detection thereof

INVENTOR(S): Altshuler, David; Cargill, Michele; Daley, George Q.; Ireland, James S.; Lander, Eric S.; Lipshutz, Robert J.; Patil, Nila; Sklar, Pamela

PATENT ASSIGNEE(S): Whitehead Institute for Biomedical Research, USA; Affymetrix, Inc.

SOURCE: PCT Int. Appl., 216 pp.
CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
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WO 2000058519	A2	20001005	WO 2000-US8440	20000330
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RW:	GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG			
PRIORITY APPLN. INFO.:			US 1999-127248P	P 19990331

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L5 26 US 6821724/PN

(US6821724/PN)

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NEWS	3	JAN 16	CAS patent coverage enhanced to include exemplified prophetic substances
NEWS	4	JAN 28	USPATFULL, USPAT2, and USPATOLD enhanced with new custom IPC display formats
NEWS	5	JAN 28	MARPAT searching enhanced
NEWS	6	JAN 28	USGENE now provides USPTO sequence data within 3 days of publication
NEWS	7	JAN 28	TOXCENTER enhanced with reloaded MEDLINE segment
NEWS	8	JAN 28	MEDLINE and LMEDLINE reloaded with enhancements
NEWS	9	FEB 08	STN Express, Version 8.3, now available
NEWS	10	FEB 20	PCI now available as a replacement to DPCI
NEWS	11	FEB 25	IFIREF reloaded with enhancements
NEWS	12	FEB 25	IMSPRODUCT reloaded with enhancements
NEWS	13	FEB 29	WPINDEX/WPIDS/WPIX enhanced with ECLA and current U.S. National Patent Classification

NEWS 14 MAR 31 IFICDB, IFIPAT, and IFIUDB enhanced with new custom
IPC display formats

NEWS 15 MAR 31 CAS REGISTRY enhanced with additional experimental
spectra

NEWS 16 MAR 31 CA/CAPplus and CASREACT patent number format for U.S.
applications updated

NEWS 17 MAR 31 LPCI now available as a replacement to LDPCI

NEWS 18 MAR 31 EMBASE, EMBAL, and LEMBASE reloaded with enhancements

NEWS 19 APR 04 STN AnaVist, Version 1, to be discontinued

NEWS 20 APR 15 WPIDS, WPINDEX, and WPIX enhanced with new
predefined hit display formats

NEWS 21 APR 28 EMBASE Controlled Term thesaurus enhanced

NEWS 22 APR 28 IMSRESEARCH reloaded with enhancements

NEWS 23 MAY 30 INPAFAMDB now available on STN for patent family
searching

NEWS 24 MAY 30 DGENE, PCTGEN, and USGENE enhanced with new homology
sequence search option

NEWS 25 JUN 06 EPFULL enhanced with 260,000 English abstracts

NEWS 26 JUN 06 KOREAPAT updated with 41,000 documents

NEWS 27 JUN 13 USPATFULL and USPAT2 updated with 11-character
patent numbers for U.S. applications

NEWS 28 JUN 19 CAS REGISTRY includes selected substances from
web-based collections

NEWS 29 JUN 25 CA/CAPplus and USPAT databases updated with IPC
reclassification data

NEWS 30 JUN 30 AEROSPACE enhanced with more than 1 million U.S.
patent records

NEWS 31 JUN 30 EMBASE, EMBAL, and LEMBASE updated with additional
options to display authors and affiliated
organizations

NEWS 32 JUN 30 STN on the Web enhanced with new STN AnaVist
Assistant and BLAST plug-in

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NEWS EXPRESS JUNE 27 08 CURRENT WINDOWS VERSION IS V8.3,
AND CURRENT DISCOVER FILE IS DATED 23 JUNE 2008.

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COST IN U.S. DOLLARS	SINCE FILE	TOTAL
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FULL ESTIMATED COST	0.21	0.21

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STRUCTURE FILE UPDATES: 20 JUL 2008 HIGHEST RN 1035004-20-6
DICTIONARY FILE UPDATES: 20 JUL 2008 HIGHEST RN 1035004-20-6

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=> s ATGAAATGCTCAGAT/sqsn
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=> s TGAATGAAATGCTCA/sqsn
L5 144 TGAATGAAATGCTCA/SQSN

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L6 493 L1 OR L2 OR L3 OR L4 OR L5

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8681680 SQL<=50
L7 1 L6 AND SQL<=50

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FULL ESTIMATED COST	162.67	162.88

FILE 'CAPLUS' ENTERED AT 14:14:59 ON 21 JUL 2008
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FILE COVERS 1907 - 21 Jul 2008 VOL 149 ISS 4
FILE LAST UPDATED: 20 Jul 2008 (20080720/ED)

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=> s 17

L8 1 L7

=> d ibib abs

L8 ANSWER 1 OF 1 CAPLUS COPYRIGHT 2008 ACS on STN
ACCESSION NUMBER: 2007:1280786 CAPLUS
DOCUMENT NUMBER: 148:25140
TITLE: Detecting cytochrome 3A gene by nucleic acid
hybridization using biochip
INVENTOR(S): Sheng, Haihui; Xiao, Huasheng
PATENT ASSIGNEE(S): Shanghai Biochip Co., Ltd., Peop. Rep. China
SOURCE: Faming Zhuanli Shenqing Gongkai Shuomingshu, 39pp.
CODEN: CNXXEV
DOCUMENT TYPE: Patent
LANGUAGE: Chinese
FAMILY ACC. NUM. COUNT: 2
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
CN 101067149	A	20071107	CN 2006-10119553	20061213
WO 2008011787	A1	20080131	WO 2007-CN1853	20070612
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BH, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DO, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, GT, HN, HR, HU, ID, IL, IN, IS, JP, KE, KG, KM, KN, KP, KR, KZ, LA, LC, LK, LR, LS, LT, LU, LY, MA, MD, MG, MK, MN, MW, MX, MY, MZ, NA, NG, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RS, RU, SC, SD, SE, SG, SK, SL, SM, SV, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, ZA, ZM, ZW			
RW:	AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IS, IT, LT, LU, LV, MC, MT, NL, PL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG, BW, GH, GM, KE, LS, MW, MZ, NA, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			

PRIORITY APPLN. INFO.: CN 2006-10029005 A 20060717
CN 2006-10119553 A 20061213

AB This invention relates to a method for detecting the cytochrome 3A gene in species, including human, by nucleic acid hybridization using CYT3A gene-specific biochips. The probes can hybridize with nucleotide sequence and/or complementary sequence of cytochrome 3A (CYP3A) gene. The invention provides the sequences of the DNA probes affixed on the chips. The CYP3A chip can be used for detecting CYP3A gene mutation in clinic, typing CYP3A4, CYP3A5 and CYP3A7 genes, evaluating effects of drugs.

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(FILE 'HOME' ENTERED AT 14:07:44 ON 21 JUL 2008)

FILE 'REGISTRY' ENTERED AT 14:08:05 ON 21 JUL 2008

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8929770 PY>2000

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L10 ANSWER 1 OF 7 CAPLUS COPYRIGHT 2008 ACS on STN

ACCESSION NUMBER: 2000:767749 CAPLUS

DOCUMENT NUMBER: 133:318131

TITLE: Characterization and repeat analysis of the compact genome of the freshwater pufferfish *Tetraodon nigroviridis*

AUTHOR(S): Crollius, H. Roest; Jaillon, O.; Dasilva, C.; Ozouf-Costaz, C.; Fizames, C.; Fischer, C.; Bouneau, L.; Billault, A.; Quetier, F.; Saurin, W.; Bernot, A.; Weissenbach, J.

CORPORATE SOURCE: Genoscope, Evry, 91057, Fr.

SOURCE: Genome Research (2000), 10(7), 939-949

CODEN: GEREFS; ISSN: 1088-9051

PUBLISHER: Cold Spring Harbor Laboratory Press

DOCUMENT TYPE: Journal

LANGUAGE: English

AB *Tetraodon nigroviridis* is a freshwater pufferfish 20-30 million years distant from *Fugu rubripes*. The genome of both tetraodontiforms is compact, mostly because intergenic and intronic sequences are reduced in size compared to other vertebrate genomes. The previously uncharacterized *Tetraodon* genome is described here together with a detailed anal. of its repeat content and organization. The sequencing of 46 megabases of bacterial artificial chromosome (BAC) end sequences is reported, which represents a random DNA sample equivalent to 13% of the genome. The sequence and location of rRNA gene clusters, centromeric and subtelocentric satellite sequences were determined. Minisatellites and microsatellites were cataloged and notable differences were observed in comparison with microsatellites from *Fugu*. The genome contains homologies to all known families of transposable elements, including Ty3-gypsy, Ty1-copia, Line retrotransposons, DNA transposons, and retroviruses, although their overall abundance is <1%. This structural anal. is an important prerequisite to sequencing the *Tetraodon* genome. [This abstract record is one of 10 records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].

L10 ANSWER 2 OF 7 CAPLUS COPYRIGHT 2008 ACS on STN

ACCESSION NUMBER: 2000:767717 CAPLUS

DOCUMENT NUMBER: 133:318128

TITLE: Characterization and repeat analysis of the compact genome of the freshwater pufferfish *Tetraodon nigroviridis*

AUTHOR(S): Crollius, H. Roest; Jaillon, O.; Dasilva, C.; Ozouf-Costaz, C.; Fizames, C.; Fischer, C.; Bouneau, L.; Billault, A.; Quetier, F.; Saurin, W.; Bernot, A.; Weissenbach, J.

CORPORATE SOURCE: Genoscope, Evry, 91057, Fr.

SOURCE: Genome Research (2000), 10(7), 939-949
CODEN: GEREFS; ISSN: 1088-9051

PUBLISHER: Cold Spring Harbor Laboratory Press

DOCUMENT TYPE: Journal

LANGUAGE: English

AB *Tetraodon nigroviridis* is a freshwater pufferfish 20-30 million years distant from *Fugu rubripes*. The genome of both tetraodontiforms is compact, mostly because intergenic and intronic sequences are reduced in size compared to other vertebrate genomes. The previously uncharacterized *Tetraodon* genome is described here together with a detailed anal. of its repeat content and organization. The sequencing of 46 megabases of bacterial artificial chromosome (BAC) end sequences is reported, which represents a random DNA sample equivalent to 13% of the genome. The sequence and location of rRNA gene clusters, centromeric and subtelocentric satellite sequences were determined. Minisatellites and microsatellites were cataloged and notable differences were observed in comparison with microsatellites from *Fugu*. The genome contains homologies to all known families of transposable elements, including Ty3-gypsy, Ty1-copia, Line retrotransposons, DNA transposons, and retroviruses, although their overall abundance is <1%. This structural anal. is an important prerequisite to sequencing the *Tetraodon* genome. [This abstract record is one of 10 records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].

L10 ANSWER 3 OF 7 CAPLUS COPYRIGHT 2008 ACS on STN

ACCESSION NUMBER: 2000:611831 CAPLUS

DOCUMENT NUMBER: 133:233401

TITLE: A sea urchin genome project: sequence scan, virtual map, and additional resources

AUTHOR(S): Cameron, R. Andrew; Mahairas, Gregory; Rast, Jonathan P.; Martinez, Pedro; Biondi, Ted R.; Swartzell, Steven; Wallace, James C.; Poustka, Albert J.; Livingston, Brian T.; Wray, Gregory A.; Etensohn, Charles A.; Lehrach, Hans; Britten, Roy J.; Davidson, Eric H.; Hood, Leroy

CORPORATE SOURCE: Stowers Inst. Med. Res., Kansas City, MO, 64110, USA

SOURCE: Proceedings of the National Academy of Sciences of the United States of America (2000), 97(17), 9514-9518
CODEN: PNASA6; ISSN: 0027-8424

PUBLISHER: National Academy of Sciences

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Results of a first-stage Sea Urchin Genome Project are summarized. The species chosen was *Strongylocentrotus purpuratus*, a research model of major importance in developmental and mol. biol. A virtual map of the genome was constructed by sequencing the ends of 76,020 bacterial artificial chromosome (BAC) recombinants (average length, 125 kb). The BAC-end sequence tag connectors (STCs) occur an average of 10 kb apart, and, together with restriction digest patterns recorded for the same BAC clones, they provide immediate access to contigs of several hundred kilobases surrounding any gene of interest. The STCs survey >5% of the genome and provide the estimate that this genome contains ≈27,350 protein-coding genes. The frequency distribution and canonical sequences

of all middle and highly repetitive sequence families in the genome were obtained from the STCs as well. The 500-kb Hox gene complex of this species is being sequenced in its entirety. In addition, arrayed cDNA libraries of >105 clones each were constructed from every major stage of embryogenesis, several individual cell types, and adult tissues and are available to the community. The accumulated STC data (AZ135866-AZ211804) and an expanding expressed sequence tag database (at present including >12,000 sequences) have been reported to GenBank and are accessible on public web sites. [This abstract record is one of 19 records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].

L10 ANSWER 4 OF 7 CAPLUS COPYRIGHT 2008 ACS on STN

ACCESSION NUMBER: 2000:366621 CAPLUS
DOCUMENT NUMBER: 132:344010
TITLE: The DNA sequence of human chromosome 21
AUTHOR(S): Hattori, M.; Fujiyama, A.; Taylor, T. D.; Watanabe, H.; Yada, T.; Park, H.-S.; Toyoda, A.; Ishii, K.; Totoki, Y.; Choi, D.-K.; Soeda, E.; Ohki, M.; Takagi, T.; Sakaki, Y.; Taudien, S.; Blechschmidt, K.; Polley, A.; Menzel, U.; Delabar, J.; Kumpf, K.; Lehmann, R.; Patterson, D.; Reichwald, K.; Rump, A.; Schillhabel, M.; Schudy, A.; Zimmermann, W.; Rosenthal, A.; Kudoh, J.; Shibuya, K.; Kawasaki, K.; Asakawa, S.; Shintani, A.; Sasaki, T.; Nagamine, K.; Mitsuyama, S.; Antonarakis, S. E.; Minoshima, S.; Shimizu, N.; Nordsiek, G.; Hornischer, K.; Brandt, P.; Scharfe, M.; Schon, O.; Desario, A.; Relchelt, J.; Kauer, G.; Blocker, H.; Ramser, J.; Beck, A.; Klages, S.; Hennig, S.; Riesselmann, L.; Dagand, E.; Haaf, T.; Wehrmeyer, S.; Borzym, K.; Gardiner, K.; Nizetic, D.; Francis, F.; Lehrach, H.; Reinhardt, R.; Yaspo, M.-L.
CORPORATE SOURCE: Genomic Sciences Center, RIKEN, Sagamihara, 228-8555, Japan
SOURCE: Nature (London) (2000), 405(6784), 311-319
CODEN: NATUAS; ISSN: 0028-0836
PUBLISHER: Nature Publishing Group
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Chromosome 21 is the smallest human autosome. An extra copy of chromosome 21 causes Down syndrome, the most frequent genetic cause of significant mental retardation, which affects up to 1 in 700 live births. Several anonymous loci for monogenic disorders and predispositions for common complex disorders have also been mapped to this chromosome, and loss of heterozygosity has been observed in regions associated with solid tumors. This report provides the sequence and gene catalog of the long arm of chromosome 21. At least 33,546,361 base pairs (bp) of DNA have been sequenced with very high accuracy, the largest contig being 25,491,867 bp. Only 3 small clone gaps and 7 sequencing gaps remain, comprising .apprx.100 kilobases. Thus, 99.7% coverage of 21q was achieved. About 281,116 bp were also sequenced from the short arm. The structural features identified include duplications that are probably involved in chromosomal abnormalities and repeat structures in the telomeric and pericentromeric regions. Anal. of the chromosome revealed 127 known genes, 98 predicted genes and 59 pseudogenes. The sequences are deposited in the GenBank database, and addnl. information can be found from the home pages of the participating centers of the chromosome 21 sequencing consortium.

REFERENCE COUNT: 46 THERE ARE 46 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L10 ANSWER 5 OF 7 CAPLUS COPYRIGHT 2008 ACS on STN

ACCESSION NUMBER:	2000:246921 CAPLUS
DOCUMENT NUMBER:	132:275067
TITLE:	The genome sequence of <i>Drosophila melanogaster</i>
AUTHOR(S):	Adams, Mark D.; Celniker, Susan E.; Holt, Robert A.; Evans, Cheryl A.; Gocayne, Jeannine D.; Amanatides, Peter G.; Scherer, Steven E.; Li, Peter W.; Hoskins, Roger A.; Galle, Richard F.; George, Reed A.; Lewis, Suzanna E.; Richards, Stephen; Ashburner, Michael; Henderson, Scott N.; Sutton, Granger G.; Wortman, Jennifer R.; Yandell, Mark D.; Zhang, Qing; Chen, Lin X.; Brandon, Rhonda C.; Rogers, Yu-Hui C.; Blazej, Robert G.; Champe, Mark; Pfeiffer, Barret D.; Wan, Kenneth H.; Doyle, Clare; Baxter, Evan G.; Helt, Gregg; Nelson, Catherine R.; Miklos, George L. Gabor; Abril, Josep F.; Agbayani, Anna; An, Hui-Jin; Andrews-Pfannkoch, Cynthia; Baldwin, Danita; Ballew, Richard M.; Basu, Anand; Baxendale, James; Bayraktaroglu, Leyla; Beasley, Ellen M.; Beeson, Karen Y.; Benos, P. V.; Berman, Benjamin P.; Bhandari, Deepali; Bolshakov, Slava; Borkova, Dana; Botchan, Michael R.; Bouck, John; Brokstein, Peter; Brottier, Phillipe; Burtis, Kenneth C.; Busam, Dana A.; Butler, Heather; Cadieu, Edouard; Center, Angela; Chandra, Ishwar; Cherry, J. Michael; Cawley, Simon; Dahlke, Carl; Davenport, Lionel B.; Davies, Peter; De Pablos, Beatriz; Delcher, Arthur; Deng, Zuoming; Mays, Anne Deslattes; Dew, Ian; Dietz, Suzanne M.; Dodson, Kristina; Doup, Lisa E.; Downes, Michael; Dugan-Rocha, Shannon; Dunkov, Boris C.; Dunn, Patrick; Durbin, Kenneth J.; Evangelista, Carlos C.; Ferraz, Concepcion; Ferriera, Steven; Fleischmann, Wolfgang; Foster, Carl; Gabrielian, Andrei E.; Garg, Neha S.; Gelbart, William M.; Glasser, Ken; Glodek, Anna; Gong, Fangcheng; Gorrell, J. Harley; Gu, Zhiping; Guan, Ping; Harris, Michael; Harris, Nomi L.; Harvey, Damon; Heiman, Thomas J.; Hernandez, Judith R.; Houck, Jarrett; Hostin, Damon; Houston, Kathryn A.; Howland, Timothy J.; Wei, Ming-Hui; Ibegwam, Chinyere; Jalali, Mena; Kalush, Francis; Karpen, Gary H.; Ke, Zhaoxi; Kennison, James A.; Ketchum, Karen A.; Kimmel, Bruce E.; Kodira, Chinnappa D.; Kraft, Cheryl; Kravitz, Saul; Kulp, David; Lai, Zhongwu; Lasko, Paul; Lei, Yiding; Levitsky, Alexander A.; Li, Jiayin; Li, Zhenya; Liang, Yong; Lin, Xiaoying; Liu, Xiangjun; Mattei, Bettina; McIntosh, Tina C.; McLeod, Michael P.; McPherson, Duncan; Merkulov, Gennady; Milshina, Natalia V.; Mobarri, Clark; Morris, Joe; Moshrefi, Ali; Mount, Stephen M.; Moy, Mee; Murphy, Brian; Murphy, Lee; Muzny, Donna M.; Nelson, David L.; Nelson, David R.; Nelson, Keith A.; Nixon, Katherine; Nusskern, Deborah R.; Pacle, Joanne M.; Palazzolo, Michael; Pittman, Gjang S.; Pan, Sue; Pollard, John; Puri, Vinita; Reese, Martin G.; Reinert, Knut; Remington, Karin; Saunders, Robert D. C.; Scheeler, Frederick; Shen, Hua; Shue, Bixiang Christopher; Siden-Kiamos, Inga; Simpson, Michael; Skupski, Marian P.; Smith, Tom; Spier, Eugene; Spradling, Allan C.; Stapleton, Mark; Strong, Renee; Sun, Eric; Svirskas, Robert; Tector, Cyndee; Turner, Russell; Venter, Eli; Wang, Aihui H.; Wang, Xin; Wang, Zhen-Yuan; Wassarman, David A.; Weinstock, George M.; Weissenbach, Jean; Williams, Sherita M.; Woodage, Trevor; Worley, Kim C.;

Wu, David; Yang, Song; Yao, Q. Alison; Ye, Jane; Yeh, Ru-Fang; Zaveri, Jayshree S.; Zhan, Ming; Zhang, Guangren; Zhao, Qi; Zheng, Liansheng; Zheng, Xiangqun H.; Zhong, Fei N.; Zhong, Wenyan; Zhou, Xiaojun; Zhu, Shiaoping; Zhu, Xiaohong; Smith, Hamilton O.; Gibbs, Richard A.; Myers, Eugene W.; Rubin, Gerald M.; Venter, J. Craig

CORPORATE SOURCE: Celera Genomics, Rockville, MD, 20850, USA

SOURCE: Science (Washington, D. C.) (2000), 287(5461), 2185-2195

CODEN: SCIEAS; ISSN: 0036-8075

PUBLISHER: American Association for the Advancement of Science

DOCUMENT TYPE: Journal

LANGUAGE: English

AB The fly *Drosophila melanogaster* is one of the most intensively studied organisms in biol. and serves as a model system for the investigation of many developmental and cellular processes common to higher eukaryotes, including humans. The nucleotide sequence was determined of nearly all of the .apprx.120-megabase euchromatic portion of the *Drosophila* genome using a whole-genome shotgun sequencing strategy supported by extensive clone-based sequence and a high-quality bacterial artificial chromosome phys. map. Efforts are under way to close the remaining gaps; however, the sequence is of sufficient accuracy and contiguity to be declared substantially complete and to support an initial anal. of genome structure and preliminary gene annotation and interpretation. The genome encodes .apprx.13,600 genes, somewhat fewer than the smaller *Caenorhabditis elegans* genome, but with comparable functional diversity. Access to supporting information on each gene is available through FlyBase at <http://flybase.bio.indiana.edu> and through Celera at www.celera.com; the sequences are deposited in GenBank with Accession Nos. AE002566-AE003403. [This abstract record is one of 4 records for this document necessitated by the large number of index entries required to fully index the document and publication system restraints].

L10 ANSWER 6 OF 7 CAPLUS COPYRIGHT 2008 ACS on STN

ACCESSION NUMBER: 2000:246831 CAPLUS

DOCUMENT NUMBER: 132:275066

TITLE: The genome sequence of *Drosophila melanogaster*

AUTHOR(S): Adams, Mark D.; Celniker, Susan E.; Holt, Robert A.; Evans, Cheryl A.; Gocayne, Jeannine D.; Amanatides, Peter G.; Scherer, Steven E.; Li, Peter W.; Hoskins, Roger A.; Galle, Richard F.; George, Reed A.; Lewis, Suzanna E.; Richards, Stephen; Ashburner, Michael; Henderson, Scott N.; Sutton, Granger G.; Wortman, Jennifer R.; Yandell, Mark D.; Zhang, Qing; Chen, Lin X.; Brandon, Rhonda C.; Rogers, Yu-Hui C.; Blazej, Robert G.; Champe, Mark; Pfeiffer, Barret D.; Wan, Kenneth H.; Doyle, Clare; Baxter, Evan G.; Helt, Gregg; Nelson, Catherine R.; Miklos, George L. Gabor; Abril, Josep F.; Agbayani, Anna; An, Hui-Jin; Andrews-Pfannkoch, Cynthia; Baldwin, Danita; Ballew, Richard M.; Basu, Anand; Baxendale, James; Bayraktaroglu, Leyla; Beasley, Ellen M.; Beeson, Karen Y.; Benos, P. V.; Berman, Benjamin P.; Bhandari, Deepali; Bolshakov, Slava; Borkova, Dana; Botchan, Michael R.; Bouck, John; Brokstein, Peter; Brottier, Phillipe; Burtis, Kenneth C.; Busam, Dana A.; Butler, Heather; Cadieu, Edouard; Center, Angela; Chandra, Ishwar; Cherry, J. Michael; Cawley, Simon; Dahlke, Carl; Davenport, Lionel B.; Davies, Peter; De Pablos, Beatriz De; Delcher, Arthur; Deng, Zuoming; Mays, Anne Deslattes; Dew, Ian; Dietz, Suzanne M.; Dodson,

Kristina; Doup, Lisa E.; Downes, Michael; Dugan-Rocha, Shannon; Dunkov, Boris C.; Dunn, Patrick; Durbin, Kenneth J.; Evangelista, Carlos C.; Ferraz, Concepcion; Ferriera, Steven; Fleischmann, Wolfgang; Foster, Carl; Gabrielian, Andrei E.; Garg, Neha S.; Gelbart, William M.; Glasser, Ken; Glodek, Anna; Gong, Fangcheng; Gorrell, J. Harley; Gu, Zhiping; Guan, Ping; Harris, Michael; Harris, Nomi L.; Harvey, Damon; Heiman, Thomas J.; Hernandez, Judith R.; Houck, Jarrett; Hostin, Damon; Houston, Kathryn A.; Howland, Timothy J.; Wei, Ming-Hui; Ibegwam, Chinyere; Jalali, Mena; Kalush, Francis; Karpen, Gary H.; Ke, Zhaoxi; Kennison, James A.; Ketchum, Karen A.; Kimmel, Bruce E.; Kodira, Chinnappa D.; Kraft, Cheryl; Kravitz, Saul; Kulp, David; Lai, Zhongwu; Lasko, Paul; Lei, Yiding; Levitsky, Alexander A.; Li, Jiayin; Li, Zhenya; Liang, Yong; Lin, Xiaoying; Liu, Xiangjun; Mattei, Bettina; McIntosh, Tina C.; McLeod, Michael P.; McPherson, Duncan; Merkulov, Gennady; Milshina, Natalia V.; Mobarry, Clark; Morris, Joe; Moshrefi, Ali; Mount, Stephen M.; Moy, Mee; Murphy, Brian; Murphy, Lee; Muzny, Donna M.; Nelson, David L.; Nelson, David R.; Nelson, Keith A.; Nixon, Katherine; Nusskern, Deborah R.; Pacleb, Joanne M.; Palazzolo, Michael; Pittman, Gjange S.; Pan, Sue; Pollard, John; Puri, Vinita; Reese, Martin G.; Reinert, Knut; Remington, Karin; Saunders, Robert D. C.; Scheeler, Frederick; Shen, Hua; Shue, Bixiang Christopher; Siden-Kiamos, Inga; Simpson, Michael; Skupski, Marian P.; Smith, Tom; Spier, Eugene; Spradling, Allan C.; Stapleton, Mark; Strong, Renee; Sun, Eric; Svirskas, Robert; Tector, Cyndee; Turner, Russell; Venter, Eli; Wang, Aihui H.; Wang, Xin; Wang, Zhen-Yuan; Wassarman, David A.; Weinstock, George M.; Weissenbach, Jean; Williams, Sherita M.; Woodage, Trevor; Worley, Kim C.; Wu, David; Yang, Song; Yao, Q. Alison; Ye, Jane; Yeh, Ru-Fang; Zaveri, Jayshree S.; Zhan, Ming; Zhang, Guangren; Zhao, Qi; Zheng, Liansheng; Zheng, Xiangqun H.; Zhong, Fei N.; Zhong, Wenyan; Zhou, Xiaojun; Zhu, Shiaoping; Zhu, Xiaohong; Smith, Hamilton O.; Gibbs, Richard A.; Myers, Eugene W.; Rubin, Gerald M.; Venter, J. Craig

CORPORATE SOURCE: Celera Genomics, Rockville, MD, 20850, USA
 SOURCE: Science (Washington, D. C.) (2000), 287(5461), 2185-2195
 CODEN: SCIEAS; ISSN: 0036-8075
 PUBLISHER: American Association for the Advancement of Science
 DOCUMENT TYPE: Journal
 LANGUAGE: English

AB The fly *Drosophila melanogaster* is one of the most intensively studied organisms in biol. and serves as a model system for the investigation of many developmental and cellular processes common to higher eukaryotes, including humans. The nucleotide sequence was determined of nearly all of the .apprx.120-megabase euchromatic portion of the *Drosophila* genome using a whole-genome shotgun sequencing strategy supported by extensive clone-based sequence and a high-quality bacterial artificial chromosome phys. map. Efforts are under way to close the remaining gaps; however, the sequence is of sufficient accuracy and contiguity to be declared substantially complete and to support an initial anal. of genome structure and preliminary gene annotation and interpretation. The genome encodes .apprx.13,600 genes, somewhat fewer than the smaller *Caenorhabditis elegans* genome, but with comparable functional diversity. Access to

supporting information on each gene is available through FlyBase at <http://flybase.bio.indiana.edu> and through Celera at www.celera.com; the sequences are deposited in GenBank with Accession Nos. AE002566-AE003403. [This abstract record is one of 4 records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].

L10 ANSWER 7 OF 7 CAPLUS COPYRIGHT 2008 ACS on STN

ACCESSION NUMBER: 2000:47778 CAPLUS

DOCUMENT NUMBER: 132:118215

TITLE: Generation and analysis of 25 Mb of genomic DNA from the pufferfish *Fugu rubripes* by sequence scanning

AUTHOR(S): Elgar, Greg; Clark, Melody S.; Meek, Stephen; Smith, Sarah; Warner, Sarah; Edwards, Yvonne J. K.; Bouchireb, Nassima; Cottage, Amanda; Yeo, Giles S. H.; Umrana, Yagnesh; Williams, Gary; Brenner, Sydney

CORPORATE SOURCE: UK Human Genome Mapping Project (HGMP) Resource Centre, Hinxton, Cambridge, CB10 1SB, UK

SOURCE: Genome Research (1999), 9(10), 960-971

CODEN: GEREFS; ISSN: 1088-9051

PUBLISHER: Cold Spring Harbor Laboratory Press

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Over 50,000 shotgun clones were generated and analyzed from 1059 *Fugu* cosmid clones. All sequences have been minimally edited and searched against protein and DNA databases. These data are all displayed on a searchable, publicly available web site at <http://fugu.hgmp.mrc.ac.uk/>. With an average of 50 reads per cosmid, this is virtually nonredundant sequence skimming, covering 30%-50% of each clone. This essentially random data set covers nearly 25 Mb (>6%) of the *Fugu* genome and forms the basis of a series of whole genome analyses which address questions regarding gene d. and distribution in the *Fugu* genome and the similarity between *Fugu* and mammalian genes. The *Fugu* genome, with 8-fold less DNA but a similar gene repertoire, is ideally suited to this type of study because most cosmids contain more than one identifiable gene. General features of the genome are also discussed. Some estimation was made of the syntenic relationship between mammals and *Fugu* and the efficacy of ORF prediction from short, unedited *Fugu* genomic sequences studied. Comparative DNA sequence analyses are an essential tool in the functional interpretation of complex vertebrate genomes. This project highlights the utility of using the *Fugu* genome in this kind of study. [This abstract record is the third of 10 records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].

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 IABS ----- ABS, indented with text labels
 IALL ----- ALL, indented with text labels
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 ISTD ----- STD, indented with text labels

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 OIBIB ----- OBIB, indented with text labels

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 SIBIB ----- IBIB, no citations

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 HITSEQ ----- HIT RN, its text modification, its CA index name, its
 structure diagram, plus NTE and SEQ fields
 FHITSTR ----- First HIT RN, its text modification, its CA index name, and
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 FHITSEQ ----- First HIT RN, its text modification, its CA index name, its
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FILE 'REGISTRY' ENTERED AT 14:08:05 ON 21 JUL 2008

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 L2 141 S ATGAAATGCTCAGAT/SQSN
 L3 129 S AATGAAATGCTCAGA/SQSN
 L4 88 S GAATGAAATGCTCAG/SQSN
 L5 144 S TGAATGAAATGCTCA/SQSN
 L6 493 S L1 OR L2 OR L3 OR L4 OR L5
 L7 1 S L6 AND SQL<=50

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L8 1 S L7
L9 146 S L6
L10 7 S L9 NOT PY>2000

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L10 ANSWER 1 OF 7 CAPLUS COPYRIGHT 2008 ACS on STN

ACCESSION NUMBER: 2000:767749 CAPLUS

DOCUMENT NUMBER: 133:318131

TITLE: Characterization and repeat analysis of the compact genome of the freshwater pufferfish *Tetraodon nigroviridis*

AUTHOR(S): Crollius, H. Roest; Jaillon, O.; Dasilva, C.; Ozouf-Costaz, C.; Fizames, C.; Fischer, C.; Bouneau, L.; Billault, A.; Quetier, F.; Saurin, W.; Bernot, A.; Weissenbach, J.

CORPORATE SOURCE: Genoscope, Evry, 91057, Fr.

SOURCE: Genome Research (2000), 10(7), 939-949

CODEN: GEREFS; ISSN: 1088-9051

PUBLISHER: Cold Spring Harbor Laboratory Press

DOCUMENT TYPE: Journal

LANGUAGE: English

AB *Tetraodon nigroviridis* is a freshwater pufferfish 20-30 million years distant from *Fugu rubripes*. The genome of both tetraodontiforms is compact, mostly because intergenic and intronic sequences are reduced in size compared to other vertebrate genomes. The previously uncharacterized *Tetraodon* genome is described here together with a detailed anal. of its repeat content and organization. The sequencing of 46 megabases of bacterial artificial chromosome (BAC) end sequences is reported, which represents a random DNA sample equivalent to 13% of the genome. The sequence and location of rRNA gene clusters, centromeric and subtelocentric satellite sequences were determined. Minisatellites and microsatellites were cataloged and notable differences were observed in comparison with microsatellites from *Fugu*. The genome contains homologies to all known families of transposable elements, including Ty3-gypsy, Ty1-copia, Line retrotransposons, DNA transposons, and retroviruses, although their overall abundance is <1%. This structural anal. is an important prerequisite to sequencing the *Tetraodon* genome. [This abstract record is one of 10 records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].

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RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
(Biological study)

(nucleotide sequence; characterization and repeat anal. of the compact
genome of the freshwater pufferfish *Tetraodon nigroviridis*)

L10 ANSWER 2 OF 7 CAPLUS COPYRIGHT 2008 ACS on STN

ACCESSION NUMBER: 2000:767717 CAPLUS

DOCUMENT NUMBER: 133:318128

TITLE: Characterization and repeat analysis of the compact
genome of the freshwater pufferfish *Tetraodon
nigroviridis*

AUTHOR(S): Crollius, H. Roest; Jaillon, O.; Dasilva, C.;
Ozouf-Costaz, C.; Fizames, C.; Fischer, C.; Bouneau,
L.; Billault, A.; Quetier, F.; Saurin, W.; Bernot, A.;
Weissenbach, J.

CORPORATE SOURCE: Genoscope, Evry, 91057, Fr.

SOURCE: Genome Research (2000), 10(7), 939-949

CODEN: GEREFS; ISSN: 1088-9051

PUBLISHER: Cold Spring Harbor Laboratory Press

DOCUMENT TYPE: Journal

LANGUAGE: English

AB *Tetraodon nigroviridis* is a freshwater pufferfish 20-30 million years
distant from *Fugu rubripes*. The genome of both tetraodontiforms is
compact, mostly because intergenic and intronic sequences are reduced in
size compared to other vertebrate genomes. The previously uncharacterized
Tetraodon genome is described here together with a detailed anal. of its
repeat content and organization. The sequencing of 46 megabases of
bacterial artificial chromosome (BAC) end sequences is reported, which
represents a random DNA sample equivalent to 13% of the genome. The sequence
and location of rRNA gene clusters, centromeric and subtelocentric
satellite sequences were determined. Minisatellites and microsatellites were
cataloged and notable differences were observed in comparison with
microsatellites from *Fugu*. The genome contains homologies to all known
families of transposable elements, including Ty3-gypsy, Ty1-copia, Line

retrotransposons, DNA transposons, and retroviruses, although their overall abundance is <1%. This structural anal. is an important prerequisite to sequencing the Tetraodon genome. [This abstract record is one of 10 records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].

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RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)

(nucleotide sequence; characterization and repeat anal. of the compact genome of the freshwater pufferfish *Tetraodon nigroviridis*)

L10 ANSWER 3 OF 7 CAPLUS COPYRIGHT 2008 ACS on STN
 ACCESSION NUMBER: 2000:611831 CAPLUS
 DOCUMENT NUMBER: 133:233401

TITLE: A sea urchin genome project: sequence scan, virtual map, and additional resources

AUTHOR(S): Cameron, R. Andrew; Mahairas, Gregory; Rast, Jonathan P.; Martinez, Pedro; Biondi, Ted R.; Swartzell, Steven; Wallace, James C.; Poustka, Albert J.; Livingston, Brian T.; Wray, Gregory A.; Ettensohn, Charles A.; Lehrach, Hans; Britten, Roy J.; Davidson, Eric H.; Hood, Leroy

CORPORATE SOURCE: Stowers Inst. Med. Res., Kansas City, MO, 64110, USA

SOURCE: Proceedings of the National Academy of Sciences of the United States of America (2000), 97(17), 9514-9518
CODEN: PNASA6; ISSN: 0027-8424

PUBLISHER: National Academy of Sciences

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Results of a first-stage Sea Urchin Genome Project are summarized. The species chosen was *Strongylocentrotus purpuratus*, a research model of major importance in developmental and mol. biol. A virtual map of the genome was constructed by sequencing the ends of 76,020 bacterial artificial chromosome (BAC) recombinants (average length, 125 kb). The BAC-end sequence tag connectors (STCs) occur an average of 10 kb apart, and, together with restriction digest patterns recorded for the same BAC clones, they provide immediate access to contigs of several hundred kilobases surrounding any gene of interest. The STCs survey >5% of the genome and provide the estimate that this genome contains $\approx 27,350$ protein-coding genes. The frequency distribution and canonical sequences of all middle and highly repetitive sequence families in the genome were obtained from the STCs as well. The 500-kb Hox gene complex of this species is being sequenced in its entirety. In addition, arrayed cDNA libraries of >105 clones each were constructed from every major stage of embryogenesis, several individual cell types, and adult tissues and are available to the community. The accumulated STC data (AZ135866-AZ211804) and an expanding expressed sequence tag database (at present including >12,000 sequences) have been reported to GenBank and are accessible on public web sites. [This abstract record is one of 19 records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].

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RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
(Biological study)

(nucleotide sequence; sea urchin genome project including sequence
scan, virtual map, and addnl. resources)

L10 ANSWER 4 OF 7 CAPLUS COPYRIGHT 2008 ACS on STN

ACCESSION NUMBER: 2000:366621 CAPLUS

DOCUMENT NUMBER: 132:344010

TITLE: The DNA sequence of human chromosome 21

AUTHOR(S): Hattori, M.; Fujiyama, A.; Taylor, T. D.; Watanabe, H.; Yada, T.; Park, H.-S.; Toyoda, A.; Ishii, K.; Totoki, Y.; Choi, D.-K.; Soeda, E.; Ohki, M.; Takagi, T.; Sakaki, Y.; Taudlen, S.; Blechschmidt, K.; Polley, A.; Menzel, U.; Delabar, J.; Kumpf, K.; Lehmann, R.; Patterson, D.; Reichwald, K.; Rump, A.; Schillhabel, M.; Schudy, A.; Zimmermann, W.; Rosenthal, A.; Kudoh, J.; Shibuya, K.; Kawasaki, K.; Asakawa, S.; Shintani, A.; Sasaki, T.; Nagamine, K.; Mitsuyama, S.; Antonarakis, S. E.; Minoshima, S.; Shimizu, N.; Nordsiek, G.; Hornischer, K.; Brandt, P.; Scharfe, M.; Schon, O.; Desario, A.; Relchelt, J.; Kauer, G.; Blocker, H.; Ramser, J.; Beck, A.; Klages, S.; Hennig, S.; Riesselmann, L.; Dagand, E.; Haaf, T.; Wehrmeyer, S.; Borzym, K.; Gardiner, K.; Nizetic, D.; Francis, F.; Lehrach, H.; Reinhardt, R.; Yaspo, M.-L.

CORPORATE SOURCE: Genomic Sciences Center, RIKEN, Sagamihara, 228-8555, Japan

SOURCE: Nature (London) (2000), 405(6784), 311-319
CODEN: NATUAS; ISSN: 0028-0836

PUBLISHER: Nature Publishing Group

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Chromosome 21 is the smallest human autosome. An extra copy of chromosome 21 causes Down syndrome, the most frequent genetic cause of significant mental retardation, which affects up to 1 in 700 live births. Several anonymous loci for monogenic disorders and predispositions for common complex disorders have also been mapped to this chromosome, and loss of heterozygosity has been observed in regions associated with solid tumors. This report provides the sequence and gene catalog of the long arm of

chromosome 21. At least 33,546,361 base pairs (bp) of DNA have been sequenced with very high accuracy, the largest contig being 25,491,867 bp. Only 3 small clone gaps and 7 sequencing gaps remain, comprising .apprx.100 kilobases. Thus, 99.7% coverage of 21q was achieved. About 281,116 bp were also sequenced from the short arm. The structural features identified include duplications that are probably involved in chromosomal abnormalities and repeat structures in the telomeric and pericentromeric regions. Anal. of the chromosome revealed 127 known genes, 98 predicted genes and 59 pseudogenes. The sequences are deposited in the GenBank database, and addnl. information can be found from the home pages of the participating centers of the chromosome 21 sequencing consortium.

REFERENCE COUNT: 46 THERE ARE 46 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

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 RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
 (Biological study)
 (nucleotide sequence; DNA sequence of human chromosome 21)

L10 ANSWER 5 OF 7 CAPLUS COPYRIGHT 2008 ACS on STN

ACCESSION NUMBER: 2000:246921 CAPLUS

DOCUMENT NUMBER: 132:275067

TITLE: The genome sequence of *Drosophila melanogaster*

AUTHOR(S): Adams, Mark D.; Celniker, Susan E.; Holt, Robert A.;
 Evans, Cheryl A.; Gocayne, Jeannine D.; Amanatides,
 Peter G.; Scherer, Steven E.; Li, Peter W.; Hoskins,
 Roger A.; Galle, Richard F.; George, Reed A.; Lewis,
 Suzanna E.; Richards, Stephen; Ashburner, Michael;
 Henderson, Scott N.; Sutton, Granger G.; Wortman,
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 E.; Kodira, Chinnappa D.; Kraft, Cheryl; Kravitz,
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 Yiding; Levitsky, Alexander A.; Li, Jiayin; Li,
 Zhenya; Liang, Yong; Lin, Xiaoying; Liu, Xiangjun;
 Mattei, Bettina; McIntosh, Tina C.; McLeod, Michael
 P.; McPherson, Duncan; Merkulov, Gennady; Milshina,
 Natalia V.; Mobarri, Clark; Morris, Joe; Moshrefi,
 Ali; Mount, Stephen M.; Moy, Mee; Murphy, Brian;
 Murphy, Lee; Muzny, Donna M.; Nelson, David L.;
 Nelson, David R.; Nelson, Keith A.; Nixon, Katherine;
 Nusskern, Deborah R.; Pacle, Joanne M.; Palazzolo,
 Michael; Pittman, Gjang S.; Pan, Sue; Pollard, John;
 Puri, Vinita; Reese, Martin G.; Reinert, Knut;

Remington, Karin; Saunders, Robert D. C.; Scheeler, Frederick; Shen, Hua; Shue, Bixiang Christopher; Siden-Kiamos, Inga; Simpson, Michael; Skupski, Marian P.; Smith, Tom; Spier, Eugene; Spradling, Allan C.; Stapleton, Mark; Strong, Renee; Sun, Eric; Svirskas, Robert; Tector, Cyndee; Turner, Russell; Venter, Eli; Wang, Aihui H.; Wang, Xin; Wang, Zhen-Yuan; Wassarman, David A.; Weinstock, George M.; Weissenbach, Jean; Williams, Sherita M.; Woodage, Trevor; Worley, Kim C.; Wu, David; Yang, Song; Yao, Q. Alison; Ye, Jane; Yeh, Ru-Fang; Zaveri, Jayshree S.; Zhan, Ming; Zhang, Guangren; Zhao, Qi; Zheng, Liansheng; Zheng, Xiangqun H.; Zhong, Fei N.; Zhong, Wenyan; Zhou, Xiaojun; Zhu, Shiaoping; Zhu, Xiaohong; Smith, Hamilton O.; Gibbs, Richard A.; Myers, Eugene W.; Rubin, Gerald M.; Venter, J. Craig

CORPORATE SOURCE:
SOURCE:

Celera Genomics, Rockville, MD, 20850, USA
Science (Washington, D. C.) (2000), 287(5461), 2185-2195

CODEN: SCIEAS; ISSN: 0036-8075

PUBLISHER: American Association for the Advancement of Science
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The fly *Drosophila melanogaster* is one of the most intensively studied organisms in biol. and serves as a model system for the investigation of many developmental and cellular processes common to higher eukaryotes, including humans. The nucleotide sequence was determined of nearly all of the .apprx.120-megabase euchromatic portion of the *Drosophila* genome using a whole-genome shotgun sequencing strategy supported by extensive clone-based sequence and a high-quality bacterial artificial chromosome phys. map. Efforts are under way to close the remaining gaps; however, the sequence is of sufficient accuracy and contiguity to be declared substantially complete and to support an initial anal. of genome structure and preliminary gene annotation and interpretation. The genome encodes .apprx.13,600 genes, somewhat fewer than the smaller *Caenorhabditis elegans* genome, but with comparable functional diversity. Access to supporting information on each gene is available through FlyBase at <http://flybase.bio.indiana.edu> and through Celera at www.celera.com; the sequences are deposited in GenBank with Accession Nos. AE002566-AE003403. [This abstract record is one of 4 records for this document necessitated by the large number of index entries required to fully index the document and publication system restraints.].

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RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
(Biological study)

(nucleotide sequence; genome sequence of *Drosophila melanogaster*)

L10 ANSWER 6 OF 7 CAPLUS COPYRIGHT 2008 ACS on STN

ACCESSION NUMBER: 2000:246831 CAPLUS

DOCUMENT NUMBER: 132:275066

TITLE: The genome sequence of *Drosophila melanogaster*

AUTHOR(S): Adams, Mark D.; Celniker, Susan E.; Holt, Robert A.;
Evans, Cheryl A.; Gocayne, Jeannine D.; Amanatides,
Peter G.; Scherer, Steven E.; Li, Peter W.; Hoskins,
Roger A.; Galle, Richard F.; George, Reed A.; Lewis,
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CORPORATE SOURCE:

SOURCE:

Celera Genomics, Rockville, MD, 20850, USA
Science (Washington, D. C.) (2000), 287(5461), 2185-2195

CODEN: SCIEAS; ISSN: 0036-8075

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American Association for the Advancement of Science
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English

AB The fly *Drosophila melanogaster* is one of the most intensively studied organisms in biol. and serves as a model system for the investigation of many developmental and cellular processes common to higher eukaryotes, including humans. The nucleotide sequence was determined of nearly all of the .apprx.120-megabase euchromatic portion of the *Drosophila* genome using a whole-genome shotgun sequencing strategy supported by extensive clone-based sequence and a high-quality bacterial artificial chromosome phys. map. Efforts are under way to close the remaining gaps; however, the sequence is of sufficient accuracy and contiguity to be declared substantially complete and to support an initial anal. of genome structure and preliminary gene annotation and interpretation. The genome encodes .apprx.13,600 genes, somewhat fewer than the smaller *Caenorhabditis elegans* genome, but with comparable functional diversity. Access to supporting information on each gene is available through FlyBase at <http://flybase.bio.indiana.edu> and through Celera at www.celera.com; the

sequences are deposited in GenBank with Accession Nos. AE002566-AE003403.
 [This abstract record is one of 4 records for this document necessitated by
 the large number of index entries required to fully index the document and
 publication system constraints.].

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RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
 (Biological study)
 (nucleotide sequence; genome sequence of *Drosophila melanogaster*)

L10 ANSWER 7 OF 7 CAPLUS COPYRIGHT 2008 ACS on STN

ACCESSION NUMBER: 2000:47778 CAPLUS

DOCUMENT NUMBER: 132:118215

TITLE: Generation and analysis of 25 Mb of genomic DNA from
 the pufferfish *Fugu rubripes* by sequence scanning

AUTHOR(S): Elgar, Greg; Clark, Melody S.; Meek, Stephen; Smith,
 Sarah; Warner, Sarah; Edwards, Yvonne J. K.;
 Bouchireb, Nassima; Cottage, Amanda; Yeo, Giles S. H.;
 Umrana, Yagnesh; Williams, Gary; Brenner, Sydney

CORPORATE SOURCE: UK Human Genome Mapping Project (HGMP) Resource
 Centre, Hinxton, Cambridge, CB10 1SB, UK

SOURCE: Genome Research (1999), 9(10), 960-971

CODEN: GEREFS; ISSN: 1088-9051

PUBLISHER: Cold Spring Harbor Laboratory Press

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Over 50,000 shotgun clones were generated and analyzed from 1059 Fugu cosmid clones. All sequences have been minimally edited and searched against protein and DNA databases. These data are all displayed on a searchable, publicly available web site at <http://fugu.hgmp.mrc.ac.uk/>. With an average of 50 reads per cosmid, this is virtually nonredundant sequence skimming, covering 30%-50% of each clone. This essentially random data set covers nearly 25 Mb (>6%) of the Fugu genome and forms the basis of a series of whole genome analyses which address questions regarding gene d. and distribution in the Fugu genome and the similarity between Fugu and mammalian genes. The Fugu genome, with 8-fold less DNA but a similar gene repertoire, is ideally suited to this type of study because most cosmids contain more than one identifiable gene. General features of the genome are also discussed. Some estimation was made of the syntenic relationship between mammals and Fugu and the efficacy of ORF prediction from short, unedited Fugu genomic sequences studied. Comparative DNA sequence analyses are an essential tool in the functional interpretation of complex vertebrate genomes. This project highlights the utility of using the Fugu genome in this kind of study. [This abstract record is the third of 10 records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].

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RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
(Biological study)

(nucleotide sequence; generation and anal. of 25 Mb of genomic DNA from
the pufferfish *Fugu rubripes* by sequence scanning)

=> file reg

COST IN U.S. DOLLARS	SINCE FILE	TOTAL
	ENTRY	SESSION
FULL ESTIMATED COST	54.53	217.41
DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)	SINCE FILE	TOTAL
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=> s (269821-23-0 or 269536-84-7 or 271680-31-0 or 264819-97-8 or 260229-12-7 or
260226-80-0 or 197543-85-4)/rn

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1 269536-84-7/RN
1 271680-31-0/RN
1 264819-97-8/RN
1 260229-12-7/RN
1 260226-80-0/RN
1 197543-85-4/RN
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260229-12-7 OR 260226-80-0 OR 197543-85-4)/RN

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=> d his

(FILE 'HOME' ENTERED AT 14:07:44 ON 21 JUL 2008)

FILE 'REGISTRY' ENTERED AT 14:08:05 ON 21 JUL 2008

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L1 134 S TGAAATGCTCAGATT/SQSN
L2 141 S ATGAAATGCTCAGAT/SQSN
L3 129 S AATGAAATGCTCAGA/SQSN
L4 88 S GAATGAAATGCTCAG/SQSN
L5 144 S TGAATGAAATGCTCA/SQSN
L6 493 S L1 OR L2 OR L3 OR L4 OR L5
L7 1 S L6 AND SQL<=50

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FILE 'CAPLUS' ENTERED AT 14:14:59 ON 21 JUL 2008

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L8 1 S L7
L9 146 S L6
L10 7 S L9 NOT PY>2000

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FILE 'REGISTRY' ENTERED AT 14:22:49 ON 21 JUL 2008

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L11 7 S (269821-23-0 OR 269536-84-7 OR 271680-31-0 OR 264819-97-8 OR

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=> s l11 and l6

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L12 7 L11 AND L6

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=> d reg sql seq 1-7

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1 RN 271680-31-0 REGISTRY

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L12 ANSWER 1 OF 7 REGISTRY COPYRIGHT 2008 ACS on STN

SQL 811

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SEQ 1 gaggcgttcc gcgacattct tttttgtcct ctgtgacaaa tactcagact
51 gttttgtgtg aaatgctcag attagatttg ctgaattctg atattctttc
== =====
101 atatgtttct catttgtttc cagttaacat tttgtgtggt ccttgtcatg
151 tatgttgaat gttatgttga ttattgctcc tttntcacca tttttgttcc
201 tttttcacca tttttgtttt ctcttccaaa tgagggttatt actttgtttc
251 agaatgtatt taaggggaaa aaaggaaaca gtcttataaa gtgagaaaaa
301 gaatttgtgt acatgtatat caatttattt aaaacaatat gtatgtccga
351 tgtattgtat aaagagcatt caatttaaatt gttttcattg tttttaagtt
401 gataataaaa cagaaaaaaa tacaaacatg acaaaaaaat gatattggct
451 taatgacctt gttgaagata tgcttgcacg tactttcttg gcttgtatgt
501 ttagtgtgtt catacgcata gtttcttttt ttcacgccct tgtgaacatg
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651 aaaagagaaa tgttgggtggc ttgaacctat taaataaaat cacacaacat
701 gtaaaacaaa tattactatt ggcgtggata attcacagaa acactggacc
751 cnnnctatcc tctnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn
801 nnnnnnnnnn a

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HITS AT: 59-73

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2 RN 269821-23-0 REGISTRY

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L12 ANSWER 2 OF 7 REGISTRY COPYRIGHT 2008 ACS on STN

SQL 1101

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SEQ      1 aaanaacttt gaaaaacaaa cattaacaaa actacnaacg aaccttcatg
      51 aactggantc atgcagtgaa attttgactc aaaagtncaa aananaggct
     101 ctttatctgc ctctccgtca gagcttctct tcacttttat ctttcttcct
     151 catttntnca ggtgtacttc gtttatgacg aagaggtgga agaggaggag
     201 aaggatgaac ctctcccatc agaaccagtc aaaccagtca acgacaggcc
     251 tcacaagttc aaggaccact actgcaagaa gccaaaattc tgcgacgtct
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     401 ttgcctcttc agtgaacaac aagtttgcg caggtgcaa gaactgcaa
     451 accagcatcc accaccagtg ccagtcctac gtggagtcc agaggtgctt
     501 cggcaaaatt gtgagtgtca ctaaagcgca cggttgatcc aagccgccgc
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     601 gcctacagtt ctctctgta cagcagccag cagaacgcca tcgtctcaca
     651 gctgctgccc ttcggtgagt cccacacgtg cgctttgctc agttgaaact
     701 gtgttttcga cctgttgga ttttaattgtg acctcccccc ccggggggct
     751 gtttgccagc gccgtcgaa cgcaccgacc ccgtgtttga gaccctgaga
     801 atcgggtgtaa tcatggccaa caaggagcgg aagaaagggt ccgaggagaa
     851 gaagaacgtg agtcggccct cgaaaccag gatttgaact gaccacctct
     901 caaagatgtg acaaatgcac tagtgtaatt attttactca tgaaatgctc
                                     = =====
     951 agatgatgat gatgatggag gatgacgagt cgcagcccaa aaccggacga
      =====
    1001 cgacgaagga agccaaggag gtaaagacaa tcggggccana gctgagggcg
    1051 ctcacggcga caaagaggaa ctgtttcctg acagaaatgc ccctcttct
    1101 t
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HITS AT: 940-954

3 RN 269536-84-7 REGISTRY

L12 ANSWER 3 OF 7 REGISTRY COPYRIGHT 2008 ACS on STN

SQL 1018

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      51 tcatgcagtg aaattttgac tcaaaantgc aaanagagg ctctttatct
     101 gcctctccgt cagagcttct cttcactttt atctttcttc ctcatctctg
     151 caggtgtact tcgtttatga cgaagaggtg gaagaggagg agaaggatga
     201 acctcctccc atagaaccag tcaaaccagt caacgacagg cctcacaagt
     251 tcaaggacca ctactgcaag aagccaaaat tctgcgacgt ctgcgcgcgc
     301 atgatcgtgt gtacgtgcgc gacgcgtgtg ctgagcgtg gcagaggtgg
     351 tgcagaggcg acctgttcac gtgtgtccgc tctgttctgg atttgectct
     401 ttagtgaaca acaagtttgc gctcaggtgc aagaactgca aaaccagcat
     451 ccaccaccag tgccagtcct acgtggagtt ccagaggtgc ttcggcaaaa
     501 ttgtgagtg cactaaagcg cacggttgat ccaagccgcc gcaggcttta
     551 gccgntgct tctctcctcc gttagcctcc aggcttcagg agagcctaca
     601 gttctccctc tgtacagcag cccagcagaa cgccatcgtc tcacagctgc
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     751 gccagnngng ttgaangnan ngaatccgtg tttgagacc tgagaatcgg
     801 tgtaatcatg gccacaagg agcgaagaa aggttccgag gagaagaaga
     851 acgtgagttc ggccctcgaa acccaggatt tgaactgacc acctctcaa
     901 gatgtgacaa atgcactagt gtaattattt tactcatgaa atgctcagat
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HITS AT: 936-950

4 RN 264819-97-8 REGISTRY

L12 ANSWER 4 OF 7 REGISTRY COPYRIGHT 2008 ACS on STN

SQL 340000

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151	ccaaaacaca	cacacataacc	ctaaagctta	tcaaattaca	gaaaaccagg
201	gataaagaga	aaaaaaca	agcagccgca	gaatacatat	atgatgacta
251	tcatgtatca	gtcaagagat	agaaacattt	aacacgaaga	atgattcaac
301	aggaacagag	ggttccacta	acatgtaaag	agacttccga	gaacggaggc
351	gctgaggcct	cgggagaacc	tccaccgcca	ggactgagac	aacaaaccca
401	caagcgttga	gtctggatct	tgggtgagaac	ctcggaaacc	cacgtcggct
451	gagacgcagc	tctgacctga	gtggggctat	gatgtgccgg	gtggtgcagt
501	tggccaaggt	gcagcaggcc	aaggcctgag	agcaggaagc	ccggggcagg
551	agtgccagcg	agactcacc	agaagctctc	cctggggcag	gagggaggca
601	gacgccctgg	gagctggaca	gaggcaagga	agcttagcag	gaatccttcc
651	caccgtggtg	aatgaacctg	ggtgttgcta	aactcctgca	gactgtcact
701	gagagccccc	gccccacca	tgaggctggc	aggcacacac	cacggaagcc
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851	caaaggagg	tacaggagg	gcccagccca	gggtcacacg	gcagggctga
901	gaagggtgca	ctgggcacgg	agaggcaaga	cacggatagc	tggagatacc
951	gtgtgggggc	cacacatatc	tcacagtgc	catacaatca	ccctcccact
1001	atgaagcaca	aaacagggtc	caacaaatct	aaagagaggg	aagtgcagca
1051	agtatatct	gagaccacag	tgggaattaaa	accagaaacc	agaaacaaca
1101	acaaaatctg	gaggaaaacc	ctaaatgttt	ggaaattaaa	ccatacttcc
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1201	tatcacgtca	acatatatgg	ggtacaggaa	gaaacacaga	aagctctcct
1251	tcccggagg	gccctcgcg	ctggtcagct	gctgctggct	gctggcagga
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1401	tcaagggttt	ggtaagggtg	cctcagagaa	caggatcaag	gttaggtctg
1451	gatcgaaggt	gggcagtgtc	actggctccc	tgcaaaactc	cacaccacac
1501	actgtgggcc	ttccaagtgc	atcatgagcc	gccacagccg	caaacactag
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1601	aggactggca	ggatcttcta	agaaatgtgc	ataactgaga	gccagcaatt
1651	ccacgcgcaa	gtacacaccc	aacagaaatg	cttacaatg	ttccagaaga
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1751	gaaactaagg	caggaggact	gcttgaggcc	agaagttcga	gaccagcctg
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1951	ccagcctggg	taacagagca	agaccctgtc	tctaaaaata	aaaaaaaaaac
2001	agaagacagg	tgccagcatg	ttcatcactg	cactattcct	aacagccaaa
2051	ctgtggaaac	tacccaaatg	cccattgata	atagaatgaa	cgtgctgtgg
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2201	aagcggccac	agcaagaggg	aaactgaggt	caggccggcc	agcatgcctg
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2501	gttgaggctg	ctgtgagctg	agatcacacc	actgcacttc	agcctgggtg
2551	acagagttag	accgtctgga	agaaagtgtc	tagaattaaa	tacaatagat
2601	tgggtgcagt	ggctgacacc	tataatccca	gcactttggg	agtgcgaggc
2651	gagaggatca	cctgaggtca	ggagttggag	accagcctgg	caaacatggc
2701	aaaaccccat	ctctactaaa	aatacaaaaa	ttagccaggc	gtggtggcag
2751	gagcctgtaa	tccagctact	cgggaggctg	aggtaggaga	atcgcttgaa
2801	cccgggaggc	ggaggttgca	gtgaggtgga	ggttgagctg	agccgagatt
2851	gtgccaccgc	actccagcct	gggcaacaga	gcgagactct	gtctcaaaaa
2901	aaaaaaccag	atacaatgac	caaattttct	tcatcaatta	aagaggtaga
2951	acaaaagcca	aggaatgtcc	taaaagttaa	atacatagaa	actaaaaaaa
3001	taacggaaga	gagcagatta	aattgaagga	gtgagatcct	cccagatggc
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TOTAL

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SESSION

FULL ESTIMATED COST

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PASSWORD:

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COST IN U.S. DOLLARS          SINCE FILE      TOTAL
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FILE 'PCTFULL' ENTERED AT 12:15:34 ON 14 NOV 2008
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FILE LAST UPDATED: 6 NOV 2008 <20081106/UP>
FILE COVERS 1978 TO DATE

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>>> NEW FIELD UPTX, FIELD /EW NO LONGER AVAILBLE - SEE HELP CHANGE <<<

```
=> s WO0120025/pn
L1          0 WO0120025/PN
              (WO120025/PN)
```

```
=> s WO 0120025/pn
L2          0 WO 0120025/PN
              (WO120025/PN)
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=> s WO 01/20025/pn
L3          1 WO 01/20025/PN
              (WO2001020025/PN)
```

$$\Rightarrow d \text{ ibib}$$

L3	ANSWER 1 OF 1	PCTFULL	COPYRIGHT 2008 Univentio on STN
ACCESSION NUMBER:	2001020025	PCTFULL	ED 20020820
TITLE (ENGLISH):	POLYMORPHISMS IN THE HUMAN CYP3A4 AND CYP3A7 GENES AND THEIR USE IN DIAGNOSTIC AND THERAPEUTIC APPLICATIONS		
TITLE (FRENCH):	POLYMORPHISMES DANS LES GENES HUMAINS CYP3A4 ET CYP3A7 ET LEURS APPLICATIONS EN MATIERE DE DIAGNOSTIC ET DE THERAPIE		
INVENTOR(S):	WOJNOWSKI, Leszek; EISELT, Regina		
PATENT ASSIGNEE(S):	EPIDAUROS BIOTECHNOLOGIE AG; WOJNOWSKI, Leszek; EISELT, Regina		
DOCUMENT TYPE:	Patent		
PATENT INFORMATION:	NUMBER	KIND	DATE

```

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WO 2001020025          A2 20010322
DESIGNATED STATES
W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CR CU
    CZ DE DK DM DZ EE ES FI GB GD GE GH GM HR HU ID IL IN
    IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK
    MN MW MX MZ NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM
    TR TT TZ UA UG US UZ VN YU ZA ZW GH GM KE LS MW MZ SD
    SL SZ TZ UG ZW AM AZ BY KG KZ MD RU TJ TM AT BE CH CY
    DE DK ES FI FR GB GR IE IT LU MC NL PT SE BF BJ CF CG
    CI CM GA GN GW ML MR NE SN TD TG
PRIORITY INFO.: EP 1999-991 18 120.7      19990910
APPLICATION INFO.: WO 2000-EP8570      A 20000901

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=> d his

(FILE 'HOME' ENTERED AT 12:14:47 ON 14 NOV 2008)

FILE 'PCTFULL' ENTERED AT 12:15:34 ON 14 NOV 2008

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L1      0 S WO0120025/PN
L2      0 S WO 0120025/PN
L3      1 S WO 01/20025/PN

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=> s l3 and (corresponding position)
    596809 CORRESPONDING
        14 CORRESPONDINGS
    596811 CORRESPONDING
        (CORRESPONDING OR CORRESPONDINGS)
    611584 POSITION
    270164 POSITIONS
    653128 POSITION
        (POSITION OR POSITIONS)
    10079 CORRESPONDING POSITION
        (CORRESPONDING(W)POSITION)
L4      1 L3 AND (CORRESPONDING POSITION)

```

=> d ibib kwic

```

L4      ANSWER 1 OF 1      PCTFULL  COPYRIGHT 2008 Univentio on STN
ACCESSION NUMBER: 2001020025 PCTFULL ED 20020820
TITLE (ENGLISH): POLYMORPHISMS IN THE HUMAN CYP3A4 AND CYP3A7 GENES AND
                  THEIR USE IN DIAGNOSTIC AND THERAPEUTIC APPLICATIONS
TITLE (FRENCH):  POLYMORPHISMES DANS LES GENES HUMAINS CYP3A4 ET CYP3A7
                  ET LEURS APPLICATIONS EN MATIERE DE DIAGNOSTIC ET DE
                  THERAPIE
INVENTOR(S): WOJNOWSKI, Leszek;
              EISELT, Regina
PATENT ASSIGNEE(S): EPIDAUROS BIOTECHNOLOGIE AG;
                   WOJNOWSKI, Leszek;
                   EISELT, Regina
DOCUMENT TYPE: Patent
PATENT INFORMATION:

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NUMBER          KIND          DATE
-----
WO 2001020025          A2 20010322

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DESIGNATED STATES
W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CR CU
    CZ DE DK DM DZ EE ES FI GB GD GE GH GM HR HU ID IL IN
    IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK
    MN MW MX MZ NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM
    TR TT TZ UA UG US UZ VN YU ZA ZW GH GM KE LS MW MZ SD

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	SL SZ TZ UG ZW AM AZ BY KG KZ MD RU TJ TM AT BE CH CY
	DE DK ES FI FR GB GR IE IT LU MC NL PT SE BF BJ CF CG
	CI CM GA GN GW ML MR NE SN TD TG
PRIORITY INFO.:	EP 1999-991 18 120.7 19990910
APPLICATION INFO.:	WO 2000-EP8570 A 20000901
PI WO 2001020025	A2 20010322

DETD . . . may vary due to deletions or additional nucleotides or amino acids elsewhere in the gene or the polypeptide. Thus, under a corresponding position in accordance with the present invention it is to be understood that nucleotides or amino acids may differ in the indicated. . . nucleotides or amino acids which may be exchanged, deleted or comprise additional nucleotides or amino acids are also comprised by the term corresponding position . Said nucleotides or amino acids may for instance together with their neighbors form sequences which may be involved in the regulation of. . .

=>

---Logging off of STN---

=>

Executing the logoff script...

=> LOG Y

COST IN U.S. DOLLARS	SINCE FILE	TOTAL
	ENTRY	SESSION
FULL ESTIMATED COST	8.51	8.72

STN INTERNATIONAL LOGOFF AT 12:17:21 ON 14 NOV 2008

Connecting via Winsock to STN

Welcome to STN International! Enter x:x

LOGINID:SSSPTA1642BJF

PASSWORD:

TERMINAL (ENTER 1, 2, 3, OR ?):2

* * * * * Welcome to STN International * * * * *

NEWS	1	Web Page for STN Seminar Schedule - N. America
NEWS	2 JUL 28	CA/CAPplus patent coverage enhanced
NEWS	3 JUL 28	EPFULL enhanced with additional legal status information from the epoline Register

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DICTIONARY FILE UPDATES: 13 NOV 2008 HIGHEST RN 1072687-23-0

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=> s EML/SQSP
L1 206279 EML/SQSP

=> file caplus

COST IN U.S. DOLLARS	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	30.86	31.07

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=> s l1
<-----User Break----->

SEARCH ENDED BY USER

=> file reg

COST IN U.S. DOLLARS	SINCE FILE	TOTAL
	ENTRY	SESSION
FULL ESTIMATED COST	0.48	31.55

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STRUCTURE FILE UPDATES: 13 NOV 2008 HIGHEST RN 1072687-23-0
 DICTIONARY FILE UPDATES: 13 NOV 2008 HIGHEST RN 1072687-23-0

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```
=> s l1 and sql<=100
      10694085 SQL<=100
L2      7769 L1 AND SQL<=100
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COST IN U.S. DOLLARS	SINCE FILE	TOTAL
	ENTRY	SESSION
FULL ESTIMATED COST	5.61	37.16

FILE 'CAPLUS' ENTERED AT 12:36:04 ON 14 NOV 2008
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=> s 12

L3 2444 L2

=> s 13 not py>1999

10288553 PY>1999

L4 354 L3 NOT PY>1999

=> d hitseq

L4 ANSWER 1 OF 354 CAPLUS COPYRIGHT 2008 ACS on STN

IT 489078-58-2

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
(Biological study)

(amino acid sequence; genomic sequence comparison of two unrelated
isolates of the human gastric pathogen Helicobacter pylori)

RN 489078-58-2 CAPLUS

CN Protein (Helicobacter pylori strain J99 gene jhp1419) (9CI) (CA INDEX
NAME)

SEQ 1 MFEKIRKILA DIEDSQNEIE MLLKLANLSL GDFIEIKRGS MDMPKGVNEA

51 FFTQLSEEEV RLKELINALN KIKKGLLVF

=>

---Logging off of STN---

=>

Executing the logoff script...

=> LOG Y

COST IN U.S. DOLLARS

SINCE FILE

TOTAL

ENTRY

SESSION

FULL ESTIMATED COST

8.44

45.60

STN INTERNATIONAL LOGOFF AT 12:37:24 ON 14 NOV 2008

Connecting via Winsock to STN

Welcome to STN International! Enter x:x

LOGINID:SSSPTA1642BJF

PASSWORD:

TERMINAL (ENTER 1, 2, 3, OR ?):2

* * * * * Welcome to STN International * * * * *

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NEWS 2 JUL 28 CA/CAPplus patent coverage enhanced
NEWS 3 JUL 28 EPFULL enhanced with additional legal status
information from the epoline Register
NEWS 4 JUL 28 IFICDB, IFIPAT, and IFIUDB reloaded with enhancements
NEWS 5 JUL 28 STN Viewer performance improved
NEWS 6 AUG 01 INPADOCDB and INPAFAMDB coverage enhanced
NEWS 7 AUG 13 CA/CAPplus enhanced with printed Chemical Abstracts
page images from 1967-1998
NEWS 8 AUG 15 CAOLD to be discontinued on December 31, 2008
NEWS 9 AUG 15 CAPplus currency for Korean patents enhanced
NEWS 10 AUG 27 CAS definition of basic patents expanded to ensure
comprehensive access to substance and sequence
information
NEWS 11 SEP 18 Support for STN Express, Versions 6.01 and earlier,
to be discontinued
NEWS 12 SEP 25 CA/CAPplus current-awareness alert options enhanced
to accommodate supplemental CAS indexing of
exemplified prophetic substances
NEWS 13 SEP 26 WPIDS, WPINDEX, and WPIX coverage of Chinese and
and Korean patents enhanced
NEWS 14 SEP 29 IFICLS enhanced with new super search field
NEWS 15 SEP 29 EMBASE and EMBAL enhanced with new search and
display fields
NEWS 16 SEP 30 CAS patent coverage enhanced to include exemplified
prophetic substances identified in new Japanese-
language patents
NEWS 17 OCT 07 EPFULL enhanced with full implementation of EPC2000
NEWS 18 OCT 07 Multiple databases enhanced for more flexible patent
number searching
NEWS 19 OCT 22 Current-awareness alert (SDI) setup and editing
enhanced
NEWS 20 OCT 22 WPIDS, WPINDEX, and WPIX enhanced with Canadian PCT
Applications
NEWS 21 OCT 24 CHEMLIST enhanced with intermediate list of
pre-registered REACH substances

NEWS EXPRESS JUNE 27 08 CURRENT WINDOWS VERSION IS V8.3,
AND CURRENT DISCOVER FILE IS DATED 23 JUNE 2008.

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NEWS LOGIN Welcome Banner and News Items
NEWS IPC8 For general information regarding STN implementation of IPC 8

Enter NEWS followed by the item number or name to see news on that
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* * * * * STN Columbus * * * * *

FILE 'HOME' ENTERED AT 07:49:41 ON 17 NOV 2008

=> file reg

COST IN U.S. DOLLARS

SINCE FILE

TOTAL

	ENTRY	SESSION
FULL ESTIMATED COST	0.21	0.21

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DICTIONARY FILE UPDATES: 16 NOV 2008 HIGHEST RN 1072892-84-2

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=> S TGAAATGCTCAGATT/SQSN
L1 134 TGAAATGCTCAGATT/SQSN

=> S ATGAAATGCTCAGAT/SQSN
L2 142 ATGAAATGCTCAGAT/SQSN

=> S AATGAAATGCTCAGA/SQSN
L3 130 AATGAAATGCTCAGA/SQSN

=> S GAATGAAATGCTCAG/SQSN
L4 89 GAATGAAATGCTCAG/SQSN

=> S TGAATGAAATGCTCA/SQSN
L5 145 TGAATGAAATGCTCA/SQSN

=> s l1 or l2 or l3 or l4 or l5
L6 497 L1 OR L2 OR L3 OR L4 OR L5

=> s 197543-85-4/rn
L7 1 197543-85-4/RN

=> s l7 and l6
L8 1 L7 AND L6

=> d rn hit seq

L8 ANSWER 1 OF 1 REGISTRY COPYRIGHT 2008 ACS on STN
RN 197543-85-4 REGISTRY

SEQ 1 acgatcngtn anatgangga attgctccnc attncgtgta nttcantgtt
51 tccactcaat ccttttagtc tggttctctg aggcagctga tgtccaccat
101 catccagtga tcattcagcc tttgttactg cctgcatgtn gacttgtgcc
151 taaattgatt gatggcgtca ccctgcataa tgttgcncca gtttctgtgc
201 tattataaca acagccanta tgaaaccagg cngcagttgt gtcgttgata

```

251 tctaataacct ctgtgccnat gatgaccac attctttgtc cagcatatcc
301 tctgtnaatt accatthtaaa cactgtgtgt aagcnggagc aaaaactaga
351 aagagtataa tcattgaaat gctcagattc ccatctgctt ctataatttg
=====
401 tgccatatcc aaacaancta ctttcattta aacggatttg ttcattgtgtt
451 tctacncgtt agtgcccacc atttgccatg caccttgnag agccncancc
501 cactgcncgt gttctctgca caaggttncc ctggccattg gcccnga

```

HITS AT: 365-379

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SEQ      1 acgacngtn anatgangga attgctccnc attncgtgta nttcantgtt
      51 tccactcaat ctttttagtc tggttctctg aggcagctga tgtccaccat
     101 catccagtga tcattcagcc tttgttactg cctgcatgtn gacttgtgcc
     151 taaattgatt gatggcgta cctgcataa tgttgcacca gtttctgtgc
     201 tattataaca acagccanta tgaaaccagg cngcagttgt gtcgttgata
     251 tctaataacct ctgtgccnat gatgaccac attctttgtc cagcatatcc
     301 tctgtnaatt accatthtaaa cactgtgtgt aagcnggagc aaaaactaga
     351 aagagtataa tcattgaaat gctcagattc ccatctgctt ctataatttg
=====
     401 tgccatatcc aaacaancta ctttcattta aacggatttg ttcattgtgtt
     451 tctacncgtt agtgcccacc atttgccatg caccttgnag agccncancc
     501 cactgcncgt gttctctgca caaggttncc ctggccattg gcccnga

```

HITS AT: 365-379

=>